

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/722,602

DATE: 07/02/2001

TIME: 16:46:00

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\07022001\I722602.raw

P.5

ENTERED

4 <110> APPLICANT: ARNOLD, Frances H.
 5 PETROUNIA, Ionna P.
 6 SUN, Lianhong
 8 <120> TITLE OF INVENTION: DIRECTED EVOLUTION OF OXIDASE ENZYMES
 11 <130> FILE REFERENCE: 9373/1G811US1
 13 <140> CURRENT APPLICATION NUMBER: US 09/722,602
 14 <141> CURRENT FILING DATE: 2000-11-27
 16 <150> PRIOR APPLICATION NUMBER: US 09/571,553
 17 <151> PRIOR FILING DATE: 2000-05-16
 19 <160> NUMBER OF SEQ ID NOS: 36
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 36
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Primer
 31 <400> SEQUENCE: 1
 32 aattcgaagc ttatggcctc agcacctatc ggaagc 36
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 33
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Primer
 42 <400> SEQUENCE: 2
 43 cttccttcta gattactgag taacgcgaat cgt 33
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 30
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Primer
 53 <400> SEQUENCE: 3
 54 ggaagagaat tcaatacgca aaccgcctct 30
 56 <210> SEQ ID NO: 4
 57 <211> LENGTH: 32
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Primer
 64 <400> SEQUENCE: 4
 65 ggtcataagc ttttcctgtg tgaaattggt at 32
 67 <210> SEQ ID NO: 5
 68 <211> LENGTH: 30
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Artificial Sequence

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72 <220> FEATURE:
73 <223> OTHER INFORMATION: Primer
75 <400> SEQUENCE: 5
76   accatgattt cgacgtcggg accctcagca                               30
78 <210> SEQ ID NO: 6
79 <211> LENGTH: 30
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Primer
86 <400> SEQUENCE: 6
87   cttcctaagc ttctactgag taacgcgaat                               30
89 <210> SEQ ID NO: 7
90 <211> LENGTH: 30
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Primer
97 <400> SEQUENCE: 7
98   ggaagaggta ccaatacgca aaccgcctct                               30
100 <210> SEQ ID NO: 8
101 <211> LENGTH: 29
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Primer
108 <400> SEQUENCE: 8
109   ttgttcctgc ggctgcagca attgaaccg                               29
111 <210> SEQ ID NO: 9
112 <211> LENGTH: 30
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Primer
119 <400> SEQUENCE: 9
120   tgccgggtcga ctctagatta ctgagtaacg                               30
122 <210> SEQ ID NO: 10
123 <211> LENGTH: 639
124 <212> TYPE: PRT
125 <213> ORGANISM: Dactylium dendroides
127 <400> SEQUENCE: 10
128   Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
129     1           5           10           15
130   Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
131     20           25           30
132   Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
133     35           40           45
134   Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
135     50           55           60

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```

136 Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
137 65 70 75 80
138 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
139 85 90 95
140 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
141 100 105 110
142 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
143 115 120 125
144 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
145 130 135 140
146 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
147 145 150 155 160
148 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
149 165 170 175
150 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
151 180 185 190
152 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
153 195 200 205
154 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
155 210 215 220
156 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
157 225 230 235 240
158 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
159 245 250 255
160 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
161 260 265 270
162 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
163 275 280 285
164 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
165 290 295 300
166 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
167 305 310 315 320
168 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
169 325 330 335
170 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
171 340 345 350
172 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
173 355 360 365
174 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
175 370 375 380
176 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
177 385 390 395 400
178 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
179 405 410 415
180 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
181 420 425 430
182 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
183 435 440 445
184 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe

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```

185      450      455      460
186 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
187 465      470      475      480
188 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His
189      485      490      495
190 Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
191      500      505      510
192 Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
193      515      520      525
194 Thr Pro Asn Tyr Leu Tyr Asn Ser Asp Gly Asn Leu Ala Thr Arg Pro
195      530      535      540
196 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
197 545      550      555      560
198 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
199      565      570      575
200 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
201      580      585      590
202 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
203      595      600      605
204 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
205      610      615      620
206 Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
207 625      630      635
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 639
211 <212> TYPE: PRT
212 <213> ORGANISM: Dactylium dendroides
214 <400> SEQUENCE: 11
215 Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
216 1      5      10      15
217 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
218 20      25      30
219 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
220 35      40      45
221 Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
222 50      55      60
223 Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
224 65      70      75      80
225 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
226 85      90      95
227 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
228 100      105      110
229 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
230 115      120      125
231 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
232 130      135      140
233 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
234 145      150      155      160
235 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile

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```

236          165          170          175
237 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
238          180          185          190
239 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
240          195          200          205
241 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
242          210          215          220
243 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
244          225          230          235          240
245 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
246          245          250          255
247 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
248          260          265          270
249 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
250          275          280          285
251 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
252          290          295          300
253 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
254          305          310          315          320
255 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
256          325          330          335
257 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
258          340          345          350
259 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
260          355          360          365
261 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
262          370          375          380
263 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
264          385          390          395          400
265 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
266          405          410          415
267 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
268          420          425          430
269 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
270          435          440          445
271 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
272          450          455          460
273 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
274          465          470          475          480
275 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
276          485          490          495
277 Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
278          500          505          510
279 Gly Leu Ser Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
280          515          520          525
281 Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
282          530          535          540
283 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
284          545          550          555          560

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

file://C:\CRF3\Outhold\Vsri722602.htm

7/2/01

VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

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L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28